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Phylogenetic prediction and *in silico* comparative modeling of glycoprotein isolated from *nipah virus*

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Nipah virus (*NiV*) is a highly pathogenic member of the family paramyxoviridae that encodes the surface glycoprotein F and G. *Nipah virus*, a member of the genus *Henipavirus* also belong to family paramyxoviridae is highly pathogenic to many species which emerged in 1998 from pteropod fruit bats (flying foxes) and microbats of several species. *Nipah virus* (*NiV*) and Hendra virus (HeV) are newly identified members. Their recent emergence as zoonotic pathogens capable of causing illness and death in domestic animals and humans is a cause of concern. It caused an outbreak of severe respiratory disease in pigs and fatal encephalitis in humans and high mortality rate. NiV can infect a large variety of mammalian species. Transgenic cell lines were generated that expressed either the attachment protein (G) or the fusion protein (F) of NiV. Functional expression of NiV F and G was verified by complementation with the corresponding glycoprotein, which resulted in the development of syncytia. When exposed to NiV and HeV, expression of NiV G in Crandall feline kidney cells resulted in a qualitative inhibition of both cytopathic effect (CPE) and cell death by both viruses. A recombinant soluble form of the HeV attachment (G) envelope glycoprotein (sGHeV) has proven highly effective in protecting small animals from lethal NiV and HeV challenge when used as an immunogen. The phylogenetic prediction, *in-silico* comparative modeling and physicochemical characterization of the envelope glycoprotein isolated from *Nipah virus* was done using different bioinformatics tools. The assessment of generated three dimensional structures through Geno3D software against structure verification tools PROCHECK and WHATIF showed that model generated was acceptable and showed the best results in three dimensional space. The predicted model can be used in structure based drug designing and vaccine development.

Keywords: Nipah virus, glycoprotein, *in silico*, Geno3D, PROCHECK